

38-21(52806)B Sequence Listing.txt
SEQUENCE LISTING

<110> Monsanto Technology LLC

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Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Thuringiensis and Uses Therefor

<130> 38-21(52806)B

<150> PCT/US04/21692

<151> 2004-07-06

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Bacillus thuringiensis

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Val	Ala	Leu	Cys	Thr	Val	Pro	Ile	Leu	Met	Val	Ser	Thr	Phe	Ala	Ser	
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tca	agc	atg	tca	gct	ttt	gct	gca	gaa	gcc	aaa	tca	cca	gat	tta	aat	269
Ser	Ser	Met	Ser	Ala	Phe	Ala	Ala	Glu	Ala	Lys	Ser	Pro	Asp	Leu	Asn	
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Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
40 45 50 55

gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt 365
Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly

aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct 413
Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala

aga ttt tgg ata ttt aag gat caa aac aat aac cat cag aca aat aga 461
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg

ttt ata tcc tgg ttt aaa gat aat att gct agt tca aaa ggg tat aat 509
Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys Gly Tyr Asn

agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa aac gat atg 557
Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu Asn Asp Met

gat gta aca aat ata gat tat aca tct aag aca ggc gat acc att tat 605
Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr

aat ggt att tca gaa ttg aaa aat tat aca gga tca act caa aag atg 653
Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr Gln Lys Met

38-21(52806)B Sequence Listing.txt

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gta act aat gga tta caa tta gga ttt aaa gtt gct gct aaa gga gta			749
Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val			
185	190	195	
gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act tat aat cta			797
Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu			
200	205	210	215
tca act act aca act gaa aca aat aca ata tca gac aag ttt act gtc			845
Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val			
220	225	230	
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Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala Ile Val Lys			
235	240	245	
cat gat tta aga aaa atg gtt tat tct ggt act cat gat cta aag ggt			941
His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly			
250	255	260	
gat tta att gtg agt ttt aat gat aaa gag att gta caa aaa ttt att			989
Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile			
265	270	275	
tat cca aat tat aga gaa att aat tta tct gat atc cgt gaa act atg			1037
Tyr Pro Asn Tyr Arg Glu Ile Asn Leu Ser Asp Ile Arg Glu Thr Met			
280	285	290	295
att gaa att gat gaa tgg aat cat gta aac cct gtg aat ttt tat gaa			1085
Ile Glu Ile Asp Glu Trp Asn His Val Asn Pro Val Asn Phe Tyr Glu			
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315	320	325	
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Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg			
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Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Asn Pro Val Gln Thr Lys			
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<213> Bacillus thuringiensis

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38-21(52806)B Sequence Listing.txt

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
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Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
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Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu
275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn

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Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
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<212> DNA

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<222> (530)..(1621)

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atattgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact 240
gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata 300
tcttggttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgctttttt 360
tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa 420
accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgatgt 480
tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac 538
Met Lys Tyr
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Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr
5 10 15

aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg 634
Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser
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cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct 682
Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser
40 45 50

tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca 730
Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser
55 60 65

aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga 778
Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly
70 75 80

tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat 826
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38-21(52806)B Sequence Listing.txt

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aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca			922
Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala			
	120	125	130
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Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr			
	150	155	160
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	215	220	225
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	230	235	240
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	245	250	255
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Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val			
	260	265	270
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	280	285	290
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Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val Asn Thr Ile			
	295	300	305
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	325	330	335
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38-21(52806)B Sequence Listing.txt

<212> PRT

<213> *Bacillus thuringiensis*

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 35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp
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Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
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Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
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Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
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Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
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Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr
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Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro
 225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys
 Page 7

260

265

270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu
 275 280 285

Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val
 290 295 300

Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn
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 gctagaatat aaatgagagc gctaacaaaa aataatggag ggataatc atg aaa tac 177
 Met Lys Tyr
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aaa tca tca aaa gta gca ata tgt act tta tca gct tta atg ctt tca 225
 Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu Met Leu Ser
 5 10 15

aca att ggt act tcg agt atg tcc act ttt gct gca gaa aca aca tta 273
 Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu Thr Thr Leu
 20 25 30 35

cca ggt caa act ctt aag gaa caa tca ata acc cca cgt gca gaa tct 321
 Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg Ala Glu Ser
 40 45 50

tat att gat att gta caa gat aga atg aaa caa agg gat ata gaa tcg 369
 Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp Ile Glu Ser
 55 60 65

aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga 417
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38-21(52806)B Sequence Listing.txt

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100	105	110	115
aaa ggt tat gag ggt att gca gaa caa atg ggt ttg aaa ata gaa tcg			561
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gat act ata tat aat ggc gtt tcg gaa tta gaa aat aaa atg gga aca			657
Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys Met Gly Thr			
	150	155	160
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Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser			
	165	170	175
caa tca acc tca gta aca aat ggg tta caa tta gga gtt aaa gtt tct			753
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Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu Thr Ser Val			
	200	205	210
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Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr Thr Ser Asp			
	215	220	225
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Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys			
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gca gta att aag cat gat tta aga aaa atg gtg tat tct ggt acg cat			945
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260	265	270	275
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Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu Ser Asp Ile			
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Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys Asn Gly Asp			
	310	315	320
acc tta tat ata gag act cca gct aaa ttt att ttt aat gga gct aat			1185
Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn Gly Ala Asn			
	325	330	335
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340	345	350	355
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Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu			
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38-21(52806)B Sequence Listing.txt

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<213> Bacillus thuringiensis

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Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
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Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val
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Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys
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Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly
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Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys
 145 150 155 160

Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val
 180 185 190

Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu
 195 200 205

38-21(52806)B Sequence Listing.txt

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr
210 215 220

Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
225 230 235 240

Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys
260 265 270

Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu
275 280 285

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val
290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn
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Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu
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<213> Bacillus thuringiensis

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tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa 235
Met Lys Tyr Lys Ser Ser Lys
1 5

gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283
Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr

38-21(52806)B Sequence Listing.txt

10	15	20	
cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt			331
Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val			
25	30	35	
act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att			379
Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile			
40	45	50	55
gtg cac aat aga atg aaa caa aga gat att gaa tca aaa atg aca ggt			427
Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly			
	60	65	70
aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct			475
Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala			
	75	80	85
aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga			523
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg			
	90	95	100
ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat			571
Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp			
	105	110	115
agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg			619
Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met			
	120	125	130
gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat			667
Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr			
	140	145	150
aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg			715
Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met			
	155	160	165
aaa aca gat agt ttt caa aga gat tat aca aaa tcc cag tca act tca			763
Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser			
	170	175	180
atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata			811
Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile			
	185	190	195
gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta			859
Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu			
	200	205	210
tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt			907
Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val			
	220	225	230
cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa			955
Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys			
	235	240	245
cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga			1003
His Ser Leu Lys Lys Met Val Tyr Thr Ser Gly Thr His Asp Leu Lys Gly			
	250	255	260
gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att			1051
Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile			
	265	270	275
tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg			1099
Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met			
	280	285	290
aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa			1147
Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln			
	300	305	310

38-21(52806)B Sequence Listing.txt

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile
 315 320 325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr
 330 335 340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys
 345 350 355

cgt tta aat aac aaa taagtactt aaaggtaatt cattaacaat gtatccatta 1346
 Arg Leu Asn Asn Lys
 360

tataattaat ttataaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
 20 25 30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
 100 105 110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

38-21(52806)B Sequence Listing.txt

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
275 280 285

Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn
340 345 350

Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys
355 360

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in Bacillus species genes containing A or T in 3rd position

<400> 11

aataataatc atcaaacwaa t

21

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 978- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

<400> 12

attwggataw ataaattttt g

21

<210> 13

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

<220>

<221> CDS

<222> (1)..(1101)

<223>

<400> 13

atg aag aac cgc ttc agc aag gtc gcc ctc tgc acg gtg cct atc ctc 48
Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1 5 10 15

atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag 96
Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
20 25 30

gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac 144
Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35 40 45

gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac 192
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
50 55 60

aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc 240
Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac 288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc 336
Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
100 105 110

gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa 384
Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
115 120 125

38-21(52806)B Sequence Listing.txt

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atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt      432
Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
    130                      135                      140

aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat      480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
    145                      150                      155                      160

acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac      528
Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
                      165                      170                      175

aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc      576
Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
                      180                      185                      190

aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag      624
Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
                      195                      200                      205

act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca      672
Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
                      210                      215                      220

att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca      720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
    225                      230                      235                      240

ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc      768
Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
                      245                      250                      255

ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag      816
Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
                      260                      265                      270

gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc      864
Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
                      275                      280                      285

agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac gtg      912
Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
                      290                      295                      300

aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag      960
Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
    305                      310                      315                      320

aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac     1008
Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
                      325                      330                      335

gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac     1056
Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
                      340                      345                      350

aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg         1101
Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
                      355                      360                      365

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<210> 14

<211> 367

<212> PRT

<213> Artificial Sequence

<220>

38-21(52806)B Sequence Listing.txt

<223> coding sequence preferred for use in monocot species encoding a B
t TIC901 amino acid sequence variant

<400> 14

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1 5 10 15

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
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280

285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
 340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
 355 360 365

<210> 15

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

<400> 15

cctttggcag aaactttaac tcc

23

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

<400> 16

gtgtattctg gtacgcatga c

21

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

38-21(52806)B Sequence Listing.txt

mal amplification reactions

<400> 17
gccggatccc tagctgaata tgcagtagat aatg 34

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18
gtggcacgtt tataggccat tgttc 25

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19
cttttaggcc catctgttca gcg 23

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

<400> 20
gccttagccg gtgcggattt tgaagc 26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

38-21(52806)B Sequence Listing.txt

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21
ggagcttatt tgttatttaa acgctttgtt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 23
aayatgcarg arcarathat hgaygg 26

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24
aayatgcarg arcarathat hga 23

<210> 25

<211> 20

38-21(52806)B Sequence Listing.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25

aayatgcarg arcarathat

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

<220>

<221> misc_feature

<222> (3)..(3)

<223> inosine

<220>

<221> misc_feature

<222> (9)..(9)

<223> inosine

<400> 26

ggngayacna thtayaaygg

20

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:28 and SEQ ID NO:29

38-21(52806)B Sequence Listing.txt

<220>

<221> misc_feature

<222> (6)..(6)

<223> inosine

<220>

<221> misc_feature

<222> (24)..(24)

<223> inosine

<400> 27

tarttnggrt adatraaytt ytgnac

26

<210> 28

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29

<220>

<221> misc_feature

<222> (6)..(6)

<223> inosine

<400> 28

tarttnggrt adatraaytt ytg

23

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28

<220>

<221> misc_feature

<222> (18)..(18)

38-21(52806)B Sequence Listing.txt

<223> inosine

<400> 29
ggrtadatra ayttytgnac 20

<210> 30

<211> 570

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

<400> 30
ttt tta gct aga ttt tgg ata ttt gag gat caa aat aat agt cac caa 48
Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln
1 5 10 15
aca aat aga ttt att tca tgg ttt aag gat aat att gct agt tca aaa 96
Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys
20 25 30
ggg tat aat agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa 144
Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu
35 40 45
aac gat atg gat gta aca aat ata gat tat aca tct aag aca ggc gat 192
Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp
50 55 60
acc att tat aat ggt att tca gaa ttg aaa aat tat aca gga tca act 240
Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr
65 70 75 80
caa aag atg aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa 288
Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu
85 90 95
tct act tca gta act aat gga tta caa tta gga ttt aaa gtt gct gct 336
Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala
100 105 110
aaa gga gta gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act 384
Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr
115 120 125
tat aat cta tca act act aca act gaa aca aat aca ata tca gac aag 432
Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys
130 135 140
ttt act gtc cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg 480
Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala
145 150 155 160
ata gtg aaa cat gat tta aga aaa atg gtt tat tct ggt act cat gat 528
Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp
165 170 175

38-21(52806)B Sequence Listing.txt

cta aag ggt gat tta att gtg agt ttt aat gat aaa gag att 570
 Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile
 180 185 190

<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln
 1 5 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys
 20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu
 35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp
 50 55 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr
 65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu
 85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala
 100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr
 115 120 125

Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys
 130 135 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala
 145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp
 165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile
 180 185 190

<210> 32

<211> 1095

<212> DNA

<213> Bacillus thuringiensis

38-21(52806)B Sequence Listing.txt

<220>

<221> CDS

<222> (1)..(1092)

<223> sequence encoding TIC431 precursor amino acid sequence

<400> 32

atg aaa tac aag tct tca aaa gta gca atg tgt aca tta tcg gct tta	48
Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu	
1 5 10 15	
atg ctt tcg aca atc gcc act cca agt ata tct gtt ttc gct gct gaa	96
Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu	
20 25 30	
aca act gca tca cat aag gtt act aat cag caa aca att gca cag cgt	144
Thr Thr Ala Ser His Lys Val Asn Gln Gln Thr Ile Ala Gln Arg	
35 40 45	
gca gaa tct tat atc gat att gtg cat aat aga atg aaa aaa cga gat	192
Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp	
50 55 60	
att gaa tca aaa atg aca ggt aaa cct att aat atg caa gaa caa ata	240
Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile	
65 70 75 80	
att gat gga tgg ttt tta gct aga ttt tgg ata ttc aag gac caa aat	288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn	
85 90 95	
aat agt cac caa aca aat aga ttt att tca tgg ttt aaa gat aat tta	336
Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu	
100 105 110	
gct agt cca gga ggg tat aat agt atc gct aaa caa atg ggg tta aaa	384
Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys	
115 120 125	
ata gaa gta tta aat gat atg gat ata tca aat gta aat tat act tct	432
Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser	
130 135 140	
aag aca ggg gat act ata tat aat ggt gtt tcc gaa tta aaa aat atc	480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile	
145 150 155 160	
aca ggt aca act caa aaa atg aaa aca gat agt ttt caa aga gat tat	528
Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr	
165 170 175	
aca aaa tca cag tca act tca atc acc aat gga tta caa tta gga ttt	576
Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe	
180 185 190	
aaa gtt tct gcc aaa ggg gtg ata gct tta gca gga gca gac ttc gaa	624
Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu	
195 200 205	
gca agt gtc aac tat aat tta tcc act acc gca act gaa acc aat ata	672
Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile	
210 215 220	
ata tct gat aaa ttt acc gtt cct tca caa gaa gtt aca tta gcg cca	720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro	
225 230 235 240	
gga cat aag gcg atc gta aaa cat agt tta aag aaa atg gta tac tcc	768
Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser	

38-21(52806)B Sequence Listing.txt

245	250	255	
gga acg cat gat tta aaa gga gat tta aca att act ttt aat gat aag	816		
Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys			
260 265 270			
gat tta gtt caa aaa ttt att tat cca aat tat aaa gct att gat tta	864		
Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu			
275 280 285			
tct aat att cgt aaa gca ctg act gaa att gat gaa tgg aat cat gta	912		
Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val			
290 295 300			
aaa cct acc gat ttc tat caa tta gtt ggg aac aaa aat tat ata aaa	960		
Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys			
305 310 315 320			
aac ggg gac act tta tac atc gaa aca cct gct aaa ttc act ttg aat	1008		
Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn			
325 330 335			
gga gga aac cct tat tat aca gca acc ttt acg gaa tat gat gaa agt	1056		
Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser			
340 345 350			
gga aat caa gtc aaa aca aag cat tta agt gtc aaa taa	1095		
Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys			
355 360			

<210> 33

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu
1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
20 25 30

Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp
50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
100 105 110

Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys
115 120 125

38-21(52806)B Sequence Listing.txt

Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
 225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
 260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
 275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
 325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser
 340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys
 355 360